

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: September 2, 2003, 17:50:37 / Search time 80.4517 seconds  
(without alignments)

1662.352 Million cell updates/sec

Title: US-09-613-508B-2

Perfect score: 303

Sequence: 1

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135299

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-Fgapext=7 -Ygapop=60 -Ygapext=60 -Delop=6 -Delext=7

Database: Issued\_Patents\_NA.\*

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4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	254	83.8	1369	4	US-09-124-934A-1	Sequence 1, Appl1
2	254	83.8	1369	4	US-08-334-251D-1	Sequence 1, Appl1
3	216	71.3	913	4	US-09-561-756-22	Sequence 22, Appl1
4	216	71.3	913	4	US-09-227-721-22	Sequence 22, Appl1
5	216	71.3	2309	4	US-08-556-627A-1	Sequence 1, Appl1
6	199	65.7	1371	3	US-08-462-969B-1	Sequence 1, Appl1
7	148	48.8	2377	4	US-08-556-627A-3	Sequence 3, Appl1
8	11	3.6	1440	4	US-09-561-756-31	Sequence 31, Appl1
9	11	3.6	1440	4	US-09-227-721-31	Sequence 31, Appl1
10	11	3.6	1700	1	US-08-665-220-1	Sequence 1, Appl1
11	11	3.6	1700	3	US-09-291-692-1	Sequence 1, Appl1
12	11	3.6	1704	4	US-09-962-834A-1	Sequence 1, Appl1

13	11	3.6	2152	4	US-08-724-378D-1	Sequence 1, Appl1
14	11	3.6	3535	2	US-08-618-408B-1	Sequence 1, Appl1
15	10	3.3	639	3	US-08-852-936C-3	Sequence 3, Appl1
16	10	3.3	639	3	US-09-300-328-3	Sequence 3, Appl1
17	10	3.3	810	4	US-09-659-845A-23	Sequence 23, Appl1
18	10	3.3	835	4	US-09-561-756-10	Sequence 10, Appl1
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36	10	3.3	1177	2	US-08-890-542A-3	Sequence 3, Appl1
37	10	3.3	1251	3	US-09-257-218-1	Sequence 1, Appl1
38	10	3.3	1251	3	US-09-311-760-1	Sequence 1, Appl1
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40	10	3.3	1251	4	US-10-059-749-1	Sequence 1, Appl1
41	10	3.3	1252	4	US-09-561-756-28	Sequence 28, Appl1
42	10	3.3	1252	4	US-09-227-721-28	Sequence 28, Appl1
43	10	3.3	1255	4	US-09-659-845A-104	Sequence 104, Appl1
44	10	3.3	1297	4	US-09-484-617-10	Sequence 10, Appl1
45	10	3.3	1365	4	US-09-659-845A-10	Sequence 10, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-124-934A-1  
; Sequence 1, Application US/09124934A  
; Patent No. 6495519  
; GENERAL INFORMATION:  
; APPLICANT: He, Wei-Wu et al.  
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3  
; FILE REFERENCE: PFI40C1  
; CURRENT APPLICATION NUMBER: US/09/124,934A  
; CURRENT FILING DATE: 1994-11-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1369  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-124-934A-1

#### Alignment Scores:

Pred. No.: 1,6e-250  
Score: 254.00  
Percent Similarity: 98.34%  
Best Local Similarity: 99.34%  
Query Match: 83.83%  
Gaps: 0  
Indels: 2  
Matches: 1369  
Conservative: 302  
Mismatches: 0

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QY 1 MetAlaAspAspGlnGlyCysGleIleGluGluGlnGlyValGluAspSerAlaAsnGluAsp 20  
DB 339 ATGGGAGATGATCAAGGCTGATTGAAGACGAGGGGTTGAGGATTCAGCAATGAAAGAT 398  
QY 21 SerValAspAlaLysProAspArgSerSerPheValProSerLeuPheSerLysLys 40  
DB 399 TCAGGAGATGCTAACCCAGACCGGCTTCGCTTTGACCGTCCCTCTTCAGTAAGAGAG 458

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QY 41 LysAsnValThrMetArgSerIleLysThrThrArgAspArgValProThrTyrGlnTyr 60
Db 459 AAAATGTCACCATGCGATTCATCAAGACCAACCGGGAGCCAGATGCGCTACATATCAATAC 518
QY 61 AsnMetAsnPhenGluLysLeuGlyLysCysIleIleIleAsnAsnLysAsnPhenAspLys 80
Db 519 AACATGAATTTTGAAGAGCTGGGCAAAATGATCATTAATAAACAAGAACTTTTGATGAAA 578
QY 81 ValThrGlyMetGlyValArgAsnGlyThrAspLysAspAlaGluAlaLeuPheLysCys 100
Db 579 GTGACAGGTATGGGGGTTTCGAAGACGAAACAGAACAAAGTCCGAGGGCGCTTTCATAGTGC 638
QY 101 PheArgSerLeuGlyPheAspValIleValTyrAsnAspCysSerCysAlaLysMetGln 120
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QY 121 AspLeuLeuLysValAspGluGluAspHisThrAsnAlaAlaCysPheAlaCysIle 140
Db 699 GATCTGCTTAAAGAGCTTGAAGAGGACCATCAAAATGCCGCTGCTGCTGCTGCTGCTGCTG 758
QY 141 LeuLeuSerHisGlyGluGluAsnValIleTyrGlyLysAspGlyValThrProIleLys 160
Db 759 CTCTTAAGCATGAGAGAGAAATGTAATTTATGGAAGATGGTGTCAACCAATTAAG 818
QY 161 AspLeuThrAlaHisPheArgGlyAspArgCysLysThrLeuLeuGlyLysProLysLeu 180
Db 819 GATTTCAGAGCCCATTTAGGGGGATGATGCAAAACCTTTTAGAGAAACCCAAACATC 878
QY 181 PhePheIleGlnAlaCysArgGlyThrGluLeuAspAspAlaIleGlnAlaAspSerGly 200
Db 879 TTCTTCATTCAGGCTTTCAGAGGAGCCAGCTTGATGATGATGATGATGATGATGATGATG 938
QY 201 ProIleAsnAspThrAspAlaAsnProArgTyrLysIleProValGluAlaAspPheLeu 220
Db 939 CCCATCATATGACACAGATGCTAATCTCGATACAGATCCAGATGGAAGCTGATCTTCCTC 998
QY 221 PheAlaTyrSerThrValProGlyTyrTyrSerTyrArgSerProGlyArgGlySerTyr 240
Db 999 TTCCCTTATTCACAGGTTCCAGGCTATTTACTCGTGGAGAGCCAGAGAGAGGCTCTCGG 1058
QY 241 PheValGlnAlaLeuCysSerIleLeuGluGlnHisGlyLysAspLeuGlnIleMetGln 260
Db 1059 TTTCGTGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1117
QY 260 nileLeuThrArgValAsnAspArgValAlaArgHisPheGluSerGlnSerAspAsp 280
Db 1118 AATCTTCACAGGAGGTGATGACAGAGTTGCCAGGCACTTGAGTCTCAGTCTGATGACCC 1177
QY 280 HisPheHisGluLysGlnIleProCysValIleValSerMetLeuThrLysGluLeuTyr 300
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QY 300 rPheSerGln 303
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Alignment Scores:
Pred. No.: 1,6e-250 Length: 1369
Score: 254.00 Matches: 302
Percent Similarity: 99.34% Conservative: 0
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 83.83% Indels: 2
DB: 4 Gaps: 0

US-09-613-508b-2 (1-303) x US-08-334-251D-1 (1-1369)
QY 1 MetAlaAspAspGlnGlyCysIleGluGlnGlyValGluAspSerAlaAsnGluAsp 20
Db 339 ATGGCAGATGATCAGAGGCGTGTATTTGAAGACGAGGGGTTGAGGATTCAGCAATAGAGT 398
QY 21 SerValAspAlaLysProAspArgSerSerPheValProSerLeuPheSerLysLys 40
Db 399 TCAAGTGAATGATTAACCCAGACCGGTCCTGTTGTATGACGTCCTCTCAGTAAAGAAAG 458
QY 41 LysAsnValThrMetArgSerIleLysThrThrArgAspArgValProThrTyrGlnTyr 60
Db 459 AAAATGTCACCATGCGATTCATCAAGACCAACCGGGAGCCAGATGCGCTACATATCAATAC 518
QY 61 AsnMetAsnPhenGluLysLeuGlyLysCysIleIleIleAsnAsnLysAsnPhenAspLys 80
Db 519 AACATGAATTTTGAAGAGCTGGGCAAAATGATCATTAATAAACAAGAACTTTTGATGAAA 578
QY 81 ValThrGlyMetGlyValArgAsnGlyThrAspLysAspAlaGluAlaLeuPheLysCys 100
Db 879 GTGACAGGTATGGGGGTTTCGAAGACGAAACAGAACAAAGTCCGAGGGCGCTTTCATAGTGC 938
QY 101 PheArgSerLeuGlyPheAspValIleValTyrAsnAspCysSerCysAlaLysMetGln 120
Db 639 TTCCGAGGCTGGGGTTTGAAGATGATGTATATATATACATGCTGCTTGGCAAGATGCA 698
QY 121 AspLeuLeuLysValAspGluGluAspHisThrAsnAlaAlaCysPheAlaCysIle 140
Db 699 GATCTGCTTAAAGAGCTTGAAGAGGACCATCAAAATGCCGCTGCTGCTGCTGCTGCTGCTG 758
QY 141 LeuLeuSerHisGlyGluGluAsnValIleTyrGlyLysAspGlyValThrProIleLys 160
Db 759 CTCTTAAGCATGAGAGAGAAATGTAATTTATGGAAGATGGTGTCAACCAATTAAG 818
QY 161 AspLeuThrAlaHisPheArgGlyAspArgCysLysThrLeuLeuGlyLysProLysLeu 180
Db 819 GATTTCAGAGCCCATTTAGGGGGATGATGCAAAACCTTTTAGAGAAACCCAAACATC 878
QY 181 PhePheIleGlnAlaCysArgGlyThrGluLeuAspAspAlaIleGlnAlaAspSerGly 200
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QY 201 ProIleAsnAspThrAspAlaAsnProArgTyrLysIleProValGluAlaAspPheLeu 220
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QY 241 PheValGlnAlaLeuCysSerIleLeuGluGlnHisGlyLysAspLeuGlnIleMetGln 260
Db 1059 TTTCGTGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1117
QY 260 nileLeuThrArgValAsnAspArgValAlaArgHisPheGluSerGlnSerAspAsp 280
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QY 300 rPheSerGln 303

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Db      1238 CTTCACTCAA 1247

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; Sequence 22, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(913)
; OTHER INFORMATION: n = A,T,C or G
US-09-561-756-22

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Score:          216.00        Matches:      302
Percent Similarity: 99.34%    Conservative: 0
Best Local Similarity: 99.34%  Mismatches: 1
Query Match:     71.29%      Indels:       2
DB:              4           Gaps:            0

US-09-613-508b-2 (1-303) x US-09-561-756-22 (1-913)

QY      1      MetAlaAspAspGlnGlyCysIleGluGluGlnGlyValGluAspSerAlaAsnGluAsp 20
DB      1      ATGGCAGATGATCAGGGCTGTATTGAAGAGCAGGGGGTTGAGATTTCAGCAAAATGAGAT 60
QY      21      SerValAspAlaLysProAspArgSerSerPheValProSerLeuPheSerLysLys 40
DB      61      TCAGTGGATGCTTAAGCCAGACCGGCTCTTGTACCCCTCTTCAGTAAGAAAGAG 120
QY      41      LysAsnValThrMetArgSerIleLysThrArgAspArgValProThrTyrGlnTyr 60
DB      121     AAAAATGCCATGCAATCCATCATCAAGACACCCGGGACCAAGTCCCTACATCATGATC 180
QY      61      AsnMetAsnPheGluLysLeuGlyLysCysIleIleIleAsnAsnLysAsnPheAspLys 80
DB      181     AACATGATATTGTTGAAAAGCTGGCAAAATGATCATTAATTAACAACAAGAACTTTGATRAA 240
QY      81      ValThrGlyMetGlyValAlaArgAsnGlyThrAspLysAspAlaGluAlaLeuPheLysCys 100
DB      241     GTGACAGGATATGGCGCTTCGAAACGAAACGAAACAAATATCCGAGGGGCTCTTCAATGTC 300
QY      101     PheArgSerLeuGlyPheAspValIleValIlyzAsnAspCysSerCysAlaLysMetGln 120
DB      301     TTCGAGAGCCCTGGCTTTTGAAGTATGTCTAATAATACATGCTCTTGTGCAAGATCA 360
QY      121     AsnLeuLeuLysLysAlaSerGluGluAspHisThrAsnAlaAlaCysPheAlaCysIle 140
DB      361     GATCTGCTTAATAAAAGCTTTCGAGAGAGACCATCAATGCCCTGCTTCCGCTGCATC 420
QY      141     LeuLeuSerHisGlyGluGluAsnValIleValIlyzAsnAspGlyValThrProIleLys 160
DB      421     CTCTTAAGCCATGAGAGAAATGTAATTTATGGGAAAGATGCTGCACACCAATTAAG 480
QY      161     AsnLeuThrAlaIlePheArgGlyAspArgCysLysThrLeuLeuGluLysProLysLeu 180
DB      481     GATTGACAGCCCACTTAAAGGGGATGATGCAAAACCTTTTAAAGAAACCAAACTC 540

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QY      200     YProIleAsnAspThrAspAlaAsnProArgTyrLysIleProValGluAlaAspPheLe 220
DB      600     GCCCATCAATGACACAGATGCTATTCCTGATRAAAGATCCCAAGTGAAGCTGACTTCT 659
QY      220     uPheAlaIlyrSerThrValProGlyTyrTyrSerTrpAspSerProGlyArgGlySerTr 240
DB      660     CTTCGGCTATTCCACCGGTTCCAGGCTATTACTGCTGAGAGAGCCCGAAGAGGCTCCGG 719
QY      240     PheValGlnAlaLeuCysSerIleLeuGluGluHisGlyLysAspLeuGluIleMetGln 260
DB      720     GTTTGTCAGAGCCCTTCTGCTTCATCTCGAAGAGACGGAAGAAAGACTGGAATATCA 779
QY      260     nIleLeuThrArgValAlaAsnAspArgValAlaArgHisPheGluSerGlnSerAspAsp 280
DB      780     GATCTCACACAGGCTGATATGACAGAGTTCCAGAGCACTTGAATCTCATCTGATGACCC 839
QY      280     ohisPheHisGlyLysLysGlnIleProCysValAlaSerMetLeuThrLysGlyLeuTyr 300
DB      840     ACACCTTCATGAGAAAGACAGATCCCTGTGTGTCTCCATGCTCACCAAGAACTCTA 899
QY      300     rPheSerGln 303
DB      900     CTTCACTCAA 909

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US-09-227-721-22
; Sequence 22, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(913)
; OTHER INFORMATION: n = A,T,C or G
US-09-227-721-22

Alignment Scores:
Pred. No.:      8,076-212      Length:      913
Score:          216.00        Matches:      302
Percent Similarity: 99.34%    Conservative: 0
Best Local Similarity: 99.34%  Mismatches: 1
Query Match:     71.29%      Indels:       2
DB:              4           Gaps:            0

US-09-613-508b-2 (1-303) x US-09-227-721-22 (1-913)

QY      1      MetAlaAspAspGlnGlyCysIleGluGluGlnGlyValGluAspSerAlaAsnGluAsp 20
DB      1      ATGGCAGATGATCAGGGCTGTATTGAAGAGCAGGGGGTTGAGATTTCAGCAAAATGAGAT 60
QY      21      SerValAspAlaLysProAspArgSerSerPheValProSerLeuPheSerLysLys 40
DB      61      TCAGTGGATGCTTAAGCCAGACCGGCTCTTGTACCCCTCTTCAGTAAGAAAGAG 120
QY      41      LysAsnValThrMetArgSerIleLysThrArgAspArgValProThrTyrGlnTyr 60
DB      121     AAAAATGCCATGCAATCCATCATCAAGACACCCGGGACCAAGTCCCTACATCATGATC 180

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DB 181 AACATGATTTTGGAAAAGCTGGGCAATGCACTCATTAACAACAAGAACTTTGATTA 240
QY 81 ValThrGlyMetGlyValAlaArgAsnGlyThrAspLysAspAlaGluAlaLeuPheLysCys 100
DB 241 GTGACAGATTAAGGCGCTTGCAGAAACGAGACAGAAAGATGCGGAGCGCTCTTCAATGTC 300
QY 101 PheArgSerLeuGlyPheAspValIleValIleThrAsnAspCysSerCysAlaLysMetGln 120
DB 301 TTCCGAAAGCTGGGTTTGACGTGATTTGTATATATGCTGCTTGTGGCCAAAGATCA 360
QY 121 AspleuLeuLysLysAlaSerGlyGluAspHisThrAsnAlaAlaCysPheAlaCysIle 140
DB 361 GATCGCTTAAAGAAAGCTTCTGAGAGAGACCATACAAATGCCGCTGCTGCTGCTGCTGCT 420
QY 141 LeuLeuSerHisGlyGlyGluAsnValIleValIleThrGlyLysAspGlyValIleProIleLys 160
DB 421 CTCTTAAGCCATGGAGAAAGAAATGTAATTTATGGGAAAGATGGTGTACACCAATAAAG 480
QY 161 AspleuThrAlaHisPheArgGlyAspArgCysLysThrLeuLeuGluLysProLysLeu 180
DB 481 GATTGACAGCCCACTTTAGGGGGATGATGCAAAACCTTTAGAGAAACCCAAACTC 540
QY 181 PhePheIleGlnAlaCysArgGlyThrGluLeuAspAspAla-IleGlnAlaAspSerG 200
DB 541 TTCTTCATTCAGGCTTGGCCGAGAGACCAAGCTTATATGTC-CATCCAGGCCGCACTGGG 599
QY 200 YProIleAsnAspThrAspAlaAsnProArgTyrIleIleProValGluAlaAspPheLe 220
DB 600 GCCCATCATGACAGATGCTAAATCCCTGATACAGATCCAGTGGAAAGCTGACTTCTCT 659
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DB 660 CTTCGCCCTATTCACAGGTTTCCAGGCTATTTACTCTGTGGAGGAGCCCAAGAAAGGCTCTG 719
QY 240 PheValIleGlnAlaLeuCysSerIleLeuGluGluIleGlyLysAspLeuGluIleMetG 260
DB 720 GTTGTGGACAGCCCTCTGCTCATCTCGAGAGAGACGAAAGACCTCGAAATCATGCA 779
QY 260 LysLeuThrArgValAsnAspArgValAlaArgHisPheGluSerGlnSerAspAspPr 280
DB 780 GATCCCTCACAGGCTGAAATGACAGAGTTCAGGACCTTATGATCTGATGATGATGATG 839
QY 280 HisPheHisGlyLysLysGlnIleProCysValIleAsnMetLeuThrLysGluLeuTyr 300
DB 840 AACTTTCATGAGAGAGAGAGATCCCTGTGTGTCTTCATGCTCAGCAAGAGATCTTA 899
QY 300 PheSerGln 303
DB 900 CTTCAGTCA 909

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,627A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 44..953
US-08-556-627A-1
Alignment Scores:
Pred. No.: 1,91e-211 Length: 2309
Score: 216.00 Matches: 302
Percent Similarity: 99.34% Conservative: 0
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 71.29% Indels: 2
DB: Gaps: 0
US-09-613-508b-2 (1-303) X US-08-556-627A-1 (1-2309)
QY 1 MetAlaAspAspGlnGlyCysIleGluGluGlnGlyValGluAspSerAlaAsnGluAsp 20
DB 44 ATGGCAGATGATCAGGCGCTGATTTAGAGAGAGAGGCGGTGATGAGATTCACCAATATGAGAT 103
QY 21 SerValAspAlaLysProAspArgSerSerPheValProSerLeuPheSerLysLys 40
DB 104 TCAGTGGATGCTTAAGCCAGACCGGCTCTGTTGTATCCCTCTTCACTTAAGAGAGAG 163
QY 41 LysAsnValThrMetArgSerIleLysThrThrArgAspArgValProThrTyrGlnTyr 60
DB 164 AAAAATGTCCATGCGATTCATCAAGACCCCGGAGCGAGTGGCTTCACTATCTGATC 223
QY 61 AsnMetAsnPheGluLysLeuGlyLysCysIleIleIleAsnAsnLysAsnPheAspLys 80
DB 224 AACATGATTTTGAAGAAGCTGGGCAATGCAATCATATATAACAACAAGAACTTTGATTA 283
QY 81 ValThrGlyMetGlyValAlaArgAsnGlyThrAspLysAspAlaGluAlaLeuPheLysCys 100
DB 284 GTGACAGATTAAGGCGCTTGCAGAAACGAGACAGAAAGATGCGGAGCGCTTCAAGTGC 343
QY 101 PheArgSerLeuGlyPheAspValIleValIleThrAsnAspCysSerCysAlaLysMetGln 120
DB 344 TTCCGAAAGCTGGGTTTGACGTGATTTGTCTATATAGATGCTGCTTGTGCCAAGATGCA 403
QY 121 AspleuLeuLysLysAlaSerGlyGluAspHisThrAsnAlaAlaCysPheAlaCysIle 140
DB 404 GATCGCTTAAAGAAAGCTTCTGAGAGAGACCATACAAATGCCGCTGCTGCTGCTGCTGCT 463
QY 141 LeuLeuSerHisGlyGlyGluAsnValIleValIleThrGlyLysAspGlyValIleProIleLys 160
DB 464 CTCTTAAGCCATGGAGAAAGAAATGTAATTTATGGGAAAGATGGTGTACACCAATAAAG 523
QY 161 AspleuThrAlaHisPheArgGlyAspArgCysLysThrLeuLeuGluLysProLysLeu 180
DB 524 GATTGACAGCCCACTTTAGGGGGATGATGCAAAACCTTTTAGGAGAAACCAAACTC 583
QY 181 PhePheIleGlnAlaCysArgGlyThrGluLeuAspAspAla-IleGlnAlaAspSerG 200

```

RESULT 5  
 US-08-556-627A-1  
 Sequence 1, Application US/08556627A  
 Patent No. 6462175  
 GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emad S.  
 APPLICANT: Fernandes-Alnemri, Teresa  
 APPLICANT: Litwack, Gerald  
 APPLICANT: Armstrong, Robert  
 APPLICANT: Tomaselli, Kevin  
 TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,  
 TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122  
 COMPUTER READABLE FORM:

Db	584	TTCTTCATTAGGCTTGCCAGAGGACCGAGCTTGATGATGG-CATCCAGGCCCACTCGGG	644
Qy	200	YProIleAsnAspThrAspAlaAsnProArgTyrIysIleProValGluAlaAspPheLe	220
Db	643	GCCCATTAAGACACAGATCTTAATCTCGATACAAAGATCCAGAGGAAGCTGACTTCT	702
Qy	220	uPheAlaTyrSerThrValProGluTyrTyrSerTrpArgSerProGlyArgGlySerTr	240
Db	703	CTTGCGCTATTCCACGGCTTCAGGGCTATTACTCGTAGAGAACCCAGAGAAAGGCTCCTG	762
Qy	240	pPheValGluAlaLeuCysserTlleuGluGluHisGlyLysAspLeuGluIleMetG	260
Db	763	GTTTGTCAGAGCCCTCTGCTCCATCTCGAGAGACACGGAAAGACCTGGAGAAATCATGCA	822
Qy	260	nIleLeuThrArgValAsnAspArgValAlaArgHisPheGluSerGlnSerAspAspPr	280
Db	823	GATCCTCACACGGGTGTAATGACAGATTCGCCAGGGCACTTTGAGTGCAGCTGAGAGACC	882
Qy	280	oHisPheHisGluLysLysGlnIleProCysValValserMetLeuThrLysGluLeuTy	300
Db	883	ACACTTCACAGAGAGAGACAGATCCCTGTGTGTGTCTCCATGCTCACACAGAACTCTA	944
Qy	300	rPheSerGln	303
Db	943	CTTCAGTCAA	952

APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomasselli, Kevin  
TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,  
NUMBER OF SEQUENCES: 11  
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use  
CORRESPONDENCE ADDRESS:  
ADDRESS: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,627A  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-8901  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2377 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 590..905  
US-08-556-627A-3  
Alignment Scores:  
Pred. No.: 6,936-142 Length: 2377  
Score: 148.00 Matches: 148  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.84% Indels: 0  
Gaps: 0  
US-09-613-508B-2 (1-303) x US-08-556-627A-3 (1-2377)  
QY 1 MetaAaSPaSPGInGlyCysIleGluGluGluGluAaSPSeRAlaAaGluAaSP 20  
Db 146 ATGGCAGATGATCAGGGGTGATTTGAAGACAGGGGGTGAAGATTCAGCAATGAAT 205  
QY 21 SerValAaSPAlaIySPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSP 40  
Db 206 TCAGTGAATGCTAAGCCAGACCGGTCCTGTTGACCTCCCTCTTCACTGAAGAGAG 265  
QY 41 LysAsnValThrMetArgSerIleLysThrThrArgAspValProThrTyGlnTyr 60  
Db 266 AAAAATCTACCACTGATGCATCAACACACCCGGACCGAGTGCCTCATATCAGTAC 325  
QY 61 AsnMetAsnPhcGluLysIleuGlyLysCysIleIleIleAsnAsnLysAsnPhcAspLys 80  
Db 326 AACATGAATTTTAAAGCTGGGCAATGATCATATATAACAAAGACTTTGTATAA 385  
QY 81 ValThrGlyMetGlyValaLarGAsnGlyThrAspLysAspAlaGluAlaLeuPhcLysCys 100  
Db 386 GTACACAGATGGGCTTCACAAACGAAACGAAAGAGAGCCAGGCGCTCTTCAAGTGC 445  
QY 101 PheArgSerLeuGlyPheAspValIleValTyrAsnAspCysSerCysAlaLysMetGln 120

Db 446 TTCGAAAGCTGGGTTTGGATGATGTCTATATATGACTCTCTTGGCCAAATGCAA 505  
QY 121 AsnLeuLeuLysValaLarGAsnGlyThrAspLysAspAlaGluAlaLeuPhcLysCys 140  
Db 506 GATCGCTTAAAGCTTGAAGAGGACCATCAATATGCGGCTGCTTGGCTGATC 565  
QY 141 LeuLeuSerHisGlyGluGluAsn 148  
Db 566 CTCCTTAAGCATGAGAAAGAAAT 589  
RESULT 8  
US-09-561-756-31  
Sequence 31, Application US/09561756  
Patent No. 6376226  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140.431  
CURRENT APPLICATION NUMBER: US/09/561,756  
PRIOR FILING DATE: 2000-04-26  
PRIORITY FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 31  
LENGTH: 1440  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-561-756-31  
Alignment Scores:  
Pred. No.: 0.0575 Length: 1440  
Score: 11.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.63% Indels: 0  
Gaps: 0  
US-09-613-508B-2 (1-303) x US-09-561-756-31 (1-1440)  
QY 176 GluLysProLysLeuPhePheIleGluAlaCys 186  
Db 1042 GAAAACTTAACCTTTTCATCCAGGCTGC 1074  
RESULT 9  
US-09-227-721-31  
Sequence 31, Application US/09227721  
Patent No. 6379950  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140.431  
CURRENT APPLICATION NUMBER: US/09/227,721  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 31  
LENGTH: 1440  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-227-721-31  
Alignment Scores:  
Pred. No.: 0.0575 Length: 1440  
Score: 11.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.63% Indels: 0  
Gaps: 0

US-09-613-508B-2 (1-303) X US-09-227-721-31 (1-1440)

QY 176 GtulyPProlySleuPhePheIlegIalAcys 186  
 DB 1042 GAAAAACCTAAACTCTTTTCATCCAGGCTGC 1074

# RESULT 10

US-08-665-220-1  
 ; Sequence 1, Application US/08665220  
 ; Patent No. 5786173

## GENERAL INFORMATION:

APPLICANT: Alnemri, Emed S.  
 APPLICANT: Fernandes-Alnemri, Teresa  
 APPLICANT: Litwack, Gerald  
 APPLICANT: Armstrong, Robert  
 APPLICANT: Tomaselli, Kevin  
 TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,  
 TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/665,220  
 FILING DATE: 14-JUN-1996  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/618,408  
 FILING DATE: 19-MAR-1996  
 ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-ID 2165  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9901  
 TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1700 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

## FEATURE:

NAME/KEY: CDS  
 LOCATION: 148..1584  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..3535  
 OTHER INFORMATION: /note= "Mch4"

## US-08-665-220-1

## Alignment Scores:

Pred. No.:	0.0671	Length:	1700
Score:	11.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.63%	Indels:	0
DB:	1	Gaps:	0

US-09-613-508B-2 (1-303) X US-08-665-220-1 (1-1700)

QY 176 GtulyPProlySleuPhePheIlegIalAcys 186  
 DB 1189 GAAAAACCTAAACTCTTTTCATCCAGGCTGC 1221

# RESULT 11

US-09-291-692-1  
 ; Sequence 1, Application US/09291692  
 ; Patent No. 6287295

## GENERAL INFORMATION:

APPLICANT: Alnemri, Emed S.  
 APPLICANT: Fernandes-Alnemri, Teresa  
 APPLICANT: Litwack, Gerald  
 APPLICANT: Armstrong, Robert  
 APPLICANT: Tomaselli, Kevin  
 TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
 TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED AND BERRY  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: Use

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/291,692  
 FILING DATE: 04-13-1999  
 CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.  
 REGISTRATION NUMBER: 44,614  
 REFERENCE/DOCKET NUMBER: 480140.424C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1700 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

## FEATURE:

NAME/KEY: CDS  
 LOCATION: 148..1584  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..1700  
 OTHER INFORMATION: /note= "Mch4"

## US-09-291-692-1

## Alignment Scores:

Pred. No.:	0.0671	Length:	1700
Score:	11.00 <td>Matches:</td> <td>11</td>	Matches:	11
Percent Similarity:	100.00% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	3.63% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	3	Gaps:	0

US-09-613-508B-2 (1-303) X US-09-291-692-1 (1-1700)

QY 176 GtulyPProlySleuPhePheIlegIalAcys 186  
 DB 1189 GAAAAACCTAAACTCTTTTCATCCAGGCTGC 1221

# RESULT 12

US-09-962-834A-1  
 ; Sequence 1, Application US/09962834A  
 ; Patent No. 6586225

## GENERAL INFORMATION:

APPLICANT: Bowman, Michael  
 TITLE OF INVENTION: NOVEL PROTEASE

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,834A  
FILING DATE: 25-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/675,123  
FILING DATE: 1996-07-03  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1704 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..1683  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-962-834A-1  
Alignment Scores:  
Pred. No.: 0.0672 Length: 1704  
Score: 11.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.63% Indels: 0  
DB: 4 Gaps: 0  
US-09-613-508B-2 (1-303) x US-09-962-834A-1 (1-1704)  
QY 176 G|U|U|P|P|o|L|y|S|L|e|u|P|H|e|P|H|e|I|l|e|G|I|N|A|C|y|S 186  
Db 1291 GAAAAACCTAAACTTTTCATCCAGGCTGC 1323  
RESULT 13  
US-08-724-378D-1  
Sequence 1, Application US/08724378D  
Patent No. 6512164  
GENERAL INFORMATION:  
APPLICANT: JUAN, SHAO-CHIEH  
APPLICANT: FLETCHER, FREDERICK A.  
APPLICANT: PATTERSON, SCOTT D.  
TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE  
FILE REFERENCE: 06843-0019-00000  
CURRENT APPLICATION NUMBER: US/08/724,378D  
CURRENT FILING DATE: 1996-10-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2152  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: (170) ..(1336)  
US-08-724-378D-1  
Alignment Scores:  
Pred. No.: 0.0834 Length: 2152  
Score: 11.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.63% Indels: 0  
DB: 4 Gaps: 0  
US-09-613-508B-2 (1-303) x US-08-724-378D-1 (1-2152)  
QY 176 G|U|U|P|P|o|L|y|S|L|e|u|P|H|e|P|H|e|I|l|e|G|I|N|A|C|y|S 186  
Db 941 GAAAAACCTAAACTTTTCATCCAGGCTGC 973  
RESULT 14  
US-08-618-408B-1  
Sequence 1, Application US/08618408B  
Patent No. 5851815  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomasek, Kevin  
TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,408B  
FILING DATE: 19-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3535 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 546..1584  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..3535  
OTHER INFORMATION: /note= "Mch4"  
US-08-618-408B-1  
Alignment Scores:  
Pred. No.: 0.132 Length: 3535  
Score: 11.00 Matches: 11



Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.63% Indels: 0  
 DB: 2 Gaps: 0

US-09-613-508B-2 (1-303) x US-08-618-408B-1 (1-3535)

Qy 176 GlyProLysLeuPhePheIleGlnAlaCys 186  
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 DB 1188 GAAAGCACTTAACCTTTTTCATCCAGGCTGTC 1220

## RESULT 15

US-08-852-936C-3  
 ; Sequence 3, Application US/08852936C  
 ; Patent No. 6010878

## GENERAL INFORMATION:

APPLICANT: DIXIT, VISHVA M.  
 APPLICANT: HE, WEI-WU  
 APPLICANT: KIKLY, KRISTINE K.  
 APPLICANT: RUBEN, STEVEN M.  
 TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING  
 TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:

ADDRESS: Ratner & Prestia  
 STREET: P.O. Box 980  
 CITY: Valley Forge  
 STATE: PA  
 COUNTRY: USA

ZIP: 19482

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/852,936C

FILING DATE: 08-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/018,961

FILING DATE: 05-JUN-1996

APPLICATION NUMBER: 60/020,344

FILING DATE: 23-MAY-1996

APPLICATION NUMBER: 60/017,949

FILING DATE: 20-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: P50483-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0700

TELEX: 846169

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 639 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

Qy 177 LysProLysLeuPhePheIleGlnAlaCys 186  
 |||||  
 DB 214 AAGCCCAAGCTCTTTTCATCCAGGCTGT 243

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 Job time: 87.4517 secs

## Alignment Scores:

Pred. No.: 0.286 Length: 639  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.30% Indels: 0  
 DB: 3 Gaps: 0

US-09-613-508B-2 (1-303) x US-08-852-936C-3 (1-639)

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 2, 2003, 17:50:37; Search time 73.5483 Seconds

(without alignments)  
1662.352 Million cell updates/sec

Title: US-09-613-508B-4

Perfect score: 277

Sequence: 1 MENTENSVDSKSIKNLEPKI.....AKQIPICVSMITKELYFYH 277

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Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135299

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

## Command line parameters:

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-d=/cgn2\_1/USPTO.spool/p/US0961508/rnat/02092003/175030/10317/app.query.fasta\_1.910  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=oligo.rml -MINMATCH=0.1 -LOOPCL=0  
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-OBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6  
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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	100.0	1001	3	US-08-964-308-5
2	277	100.0	1001	3	US-08-964-313-5
3	277	100.0	1001	4	US-09-069-138-5
4	277	100.0	1158	3	US-08-591-605-1
5	277	100.0	1159	3	US-08-462-969B-3
6	277	100.0	1159	4	US-09-124-934A-3
7	277	100.0	1159	4	US-08-334-251D-3
8	277	100.0	904	4	US-09-033-287A-4
9	210	75.8	1789	4	US-09-033-287A-6
10	210	75.8	1789	4	US-09-033-287A-6
11	189	68.2	835	4	US-09-561-756-10
12	189	68.2	835	4	US-09-227-721-10

13	189	68.2	2635	4	US-09-484-617-3	Sequence 3, Appl1
14	176	63.5	1001	3	US-08-964-308-9	Sequence 9, Appl1
15	176	63.5	1001	3	US-08-964-313-9	Sequence 9, Appl1
16	176	63.5	1001	4	US-09-069-138-9	Sequence 9, Appl1
17	175	63.2	873	4	US-09-561-756-1	Sequence 1, Appl1
18	175	63.2	873	4	US-09-227-721-1	Sequence 2, Appl1
19	147	53.1	858	4	US-09-561-756-2	Sequence 1, Appl1
20	147	53.1	858	4	US-09-227-721-2	Sequence 2, Appl1
21	35	12.6	1297	4	US-09-484-617-10	Sequence 10, Appl1
22	35	10.8	1177	2	US-08-890-542A-1	Sequence 10, Appl1
23	30	10.8	1177	2	US-08-890-542A-1	Sequence 10, Appl1
24	30	10.8	1177	2	US-08-890-542A-1	Sequence 10, Appl1
25	11	4.0	53	2	US-08-800-007A-1	Sequence 1, Appl1
26	11	4.0	85	3	US-08-800-007A-5	Sequence 5, Appl1
27	11	4.0	85	3	US-09-208-966-36	Sequence 36, Appl1
28	10	3.6	90	3	US-09-208-966-32	Sequence 32, Appl1
29	10	3.6	90	3	US-09-208-966-32	Sequence 32, Appl1
30	10	3.6	913	4	US-09-561-756-22	Sequence 22, Appl1
31	10	3.6	913	4	US-09-227-721-22	Sequence 22, Appl1
32	10	3.6	1369	4	US-09-124-934A-1	Sequence 1, Appl1
33	10	3.6	1369	4	US-08-334-251D-1	Sequence 1, Appl1
34	10	3.6	1371	3	US-08-462-969B-1	Sequence 1, Appl1
35	10	3.6	2309	4	US-08-556-627A-1	Sequence 1, Appl1
36	10	3.6	2377	4	US-08-556-627A-3	Sequence 3, Appl1
37	9	3.2	47	2	US-08-800-007A-7	Sequence 7, Appl1
38	9	3.2	47	2	US-08-800-007A-7	Sequence 7, Appl1
39	9	3.2	51	2	US-08-800-007A-8	Sequence 8, Appl1
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41	9	3.2	52	2	US-08-800-007A-2	Sequence 2, Appl1
42	9	3.2	52	2	US-08-800-007A-6	Sequence 6, Appl1
43	8	2.9	25	4	US-09-484-617-11	Sequence 11, Appl1
44	8	2.9	27	4	US-09-484-617-6	Sequence 6, Appl1
45	8	2.9	883	4	US-09-561-756-19	Sequence 19, Appl1

## ALIGNMENTS

RESULT 1  
US-08-964-308-5  
Sequence 5, Application US/08964308  
Patent No. 6066715  
GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: ZAMBONI, ROBERT  
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,308  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: NORTH, ROBERT J  
REGISTRATION NUMBER: 27,366  
REFERENCE/DOCKET NUMBER: 19840 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-7262  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1001 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-964-308-5

Alignment Scores:  
 Pred. No.: 1.72e-280 Length: 1001  
 Score: 277.00 Matches: 277  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-613-508B-4 (1-277) x US-08-964-308-5 (1-1001)

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QY 21 IleHISGlySerGlySerMetAspSerGlyIleSerLeuAspAsnSerTyrIleMetAsp 40
DB 124 ATACATGGAAGCGAATCAATGACTCTGGAATATCCCTGACACAGTTAATAATGAT 183
QY 41 TyrProGluMetGlyLeuCyellelleleasnAnlysaenPheHISlysSerThrGly 60
DB 184 TATCCTGAGATGGATTATGTATATTAATTAATAAGAAATTTTCATTAAGACACTGGA 243
QY 61 MetThrSerArgSerGlyThrAspValAspAlaAsnLeuArgGluIleValGluLeuMet 80
DB 244 ATGACATCTCGGTCTGTGACAGATGTCATGACAGAAACCTCAGGAAACCTTCAGAAC 303
QY 81 LeuIleTyrGluValArgAsnIleAsnAspLeuThrArgGluGluIleValGluLeuMet 100
DB 304 TTGAATATGAAAGTGAATTAATAATATCTTACACTGAGAAATTTGGAATTTGATG 363
QY 101 ArgAspValSerIleGlyAspHISerIleAspSerSerPheValCysValLeuLeuSer 120
DB 364 CGTGAATGTTCTTAAAGAAATCAGACGCAAAAGACAGTTTGTGTTGCTCTTCTGAGC 423
QY 121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuValIleThr 140
DB 424 CATGTGAAAGAAAGAAATTAATTTTGAACAAATGACTGTGACCTGGAATAAATAACA 483
QY 141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyIleProIleValPheIleIle 160
DB 484 AACTTTTCAAGAGGGGATCGTTGTAGAAGTCTAATCTGMAAAACCAACCTTTTCATTAAT 543
QY 161 GluIleCysArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAsp 180
DB 544 CAGGCTGCTCCGTGTACAGAACTGACTGTGCAATTGACAGACAGTGGTGTGATGAT 603
QY 181 AspMetAlaCysHISlysIleProValGluAlaAspPheLeuIleValIleThrAla 200
DB 604 GACATGGGTCTCTATAAATACCAAGTGAAGCCCACTTTCTGTATGCAATCTCCACAGCA 663
QY 201 ProGlyTyrIleSerIlePheArgAsnSerIleAspIleSerTyrPheIleGlnSerLeuCys 220
DB 664 CCTGCTATATATCTTGGCGAAATTCAAAGATGGCTCCGTTCAACCGATCCCTTTGT 723
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DB 724 GCCATGCTGAAACAGTATGCGACAGACTGAAATTTATGCAATCTTTACCCGGGTATAC 783
QY 241 ArgIleValAlaThrGluPheGluSerPheSerPheAspAlaThrPheHISAlaIleVal 260
DB 784 CGAAAGGTGGCAAGAAATTTGACTCTTTTCCITTAACCTACTTTTCATGCAAGAAAGAA 843
QY 261 GluIleProCysIleValIleSerMetLeuThrIleGluLeuIleValIleThrIleHIS 277
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# RESULT 2

US-08-964-313-5  
 Sequence 5, Application US/08964313  
 Patent No. 6114132

## GENERAL INFORMATION:

APPLICANT: DESMARAIS, SYLVIE  
 APPLICANT: FRIESEN, RICHARD  
 APPLICANT: GRESSER, MICHAEL  
 APPLICANT: KENNEDY, BRIAN  
 APPLICANT: NICHOLSON, DONALD  
 APPLICANT: RAMACHANDRAN, CHIDAMBARAN  
 APPLICANT: SKOREY, KATHRYN  
 APPLICANT: FORD-HUTCHINSON, ANTHONY  
 TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
 CITY: RAHWAY  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 07065

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,313  
 FILING DATE: 04-NOV-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/030,408  
 FILING DATE: 04-NOV-1996  
 APPLICATION NUMBER: PCT/CA97/00825

FILING DATE: 03-NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DURETTE, PHILIPPE L.  
 REGISTRATION NUMBER: 35,125  
 REFERENCE/DOCKET NUMBER: 19824Y

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4568  
 TELEFAX: 732-594-4720  
 TELEX:

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1001 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-964-313-5

## Alignment Scores:

Pred. No.: 1.72e-280 Length: 1001  
 Score: 277.00 Matches: 277  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-613-508B-4 (1-277) x US-08-964-313-5 (1-1001)

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QY 1 MetGluAsnThrGluAsnSerValAspSerIleValAsnLeuGluProIle 20
DB 64 ATGGAGAACACTGAAACCTCAGTGAATTCATAAATCGAATTTGAAACCAAGATC 123
QY 21 IleHISGlySerGlySerMetAspSerGlyIleSerLeuAspAsnSerTyrIleMetAsp 40
DB 124 ATACATGGAAGCGAATCAATGACTCTGGAATATCCCTGACACAGTTAATAATGAT 183
QY 41 TyrProGluMetGlyLeuCyellelleleasnAnlysaenPheHISlysSerThrGly 60

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Db      724  GCCATGCTGGAACAGTATGCCGACAGCTTGAATTATATGACATCTTACCCGGGTAAc 783
Oy      241  ArgLyValAlaIatrnGluPheGluSerPheSerPheAspIatrnPheHisAlaLySly 260
Db      784  CGAAAGCTGGCAACAGATTTGAGTCTCTTTCCCTTTAGCGTACTTTTCATGCAAGAA 843
Oy      261  GlnIleProCySileValSerMetLeuThrLySleuLeuYrPheYrHis 277
Db      844  CAGATTCATGATGTTTCATGCTCTCGAAGAACTCATTTTATTCAC 894

RESULT 4
US-08-591-605-1
Sequence 1, Application US/08591605
Patent No. 6060238
GENERAL INFORMATION:
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,605
FILING DATE: 09-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-21036.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 224..1054
OTHER INFORMATION: /product= "Yama peptide sequence"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 704..718
OTHER INFORMATION: /note= "region coding for
OTHER INFORMATION: pentapeptide, wherein cysteine is catalytic"
FEATURE:
NAME/KEY: mutation
LOCATION: replace(710..712, "atg")
OTHER INFORMATION: /note= "Mutation of catalytic cysteine to methionine"
FEATURE:
NAME/KEY: mutation
LOCATION: replace(710..712, "ggc")
OTHER INFORMATION: /note= "Mutation of catalytic cysteine to alanine"
FEATURE:
NAME/KEY: mutation

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/	NAME/KEY: mutation	
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/	LOCATION: replace(710..712, "gcaa")	
/	OTHER INFORMATION: /note="mutation of catalytic cysteine to alanine"	
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Score:	277.00	277
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
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DB	284 ATACGTGAAACGAAATCATGACCTCGAAATATCCCTGGAACAACAGTTATTAATTAATGAT	343
QY	41 TyrProGluMetGlyLeuGlyValIleIleIleAsnIlyAsnPheIlySerThrGly	60
DB	344 TATCCTGAGATCGGTTATGTATATATATATATATTAATTAAGATTTTCAATAAGCACTGCA	403
QY	61 MetHisSerArgSerGlyThrAspValAspAlaIleAsnLeuArgGluThrPheArgAsn	80
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DB	464 TTGAATATATGAAAGTCAGGAATTAATAATATCTTACACGTGAAGAAATTTGTGAATTTGATG	523
QY	101 ArgAspValSerIlyGluAspHisSerIlyAspSerSerPheValCysValLeuLeuSer	120
DB	524 CGTATATGTTTAAAGAAGATCAAGCAAGCAAGCAAGTGTGTTGTTGTGCTTGAGC	583
QY	121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuIlySylIleThr	140
DB	584 CATGCTGAAGAAAGAAATTAATTTTGGAAACAATGACCTGTTGACTGAATAAAAAATAACA	643
QY	141 AsnAspPheArgIlyAspArgCysArgSerLeuThrGlyIlyProIlyLeuPheIleIle	160
DB	644 AACTTTTTCAGAGGGGACCTGTTAGAAAGTCTTAAGTGAAGAAACCAAACTTTTCAATTT	703
QY	161 GluIlyIleCysArgGlyThrGluLeuAspCysGlyIlyIleGluThrAspSerGlyValAspAsp	180
DB	704 CAGCGCTCGCGTGGTGAAGAACTGACCTGCTGACCTGGAAGAAAGTGTGTGATGAT	763
QY	181 AspMetIleCysHisIlySylIleProValGluIlyAspPheLeuTyrAlaTyrSerThrIle	200
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DB	824 CTTGTTATTAATTTCTTGCGCAAAATTCAAAGATGGCTCTCGTTCATCAGTCGCTTTGT	883
QY	221 AlaMetLeuIlySerGluTyrAlaAspIlyLeuGluIlePheMetHisIleLeuThrArgValAsn	240
DB	884 GCCATGCTGAACAACGATCCCGAACAAGCTTGAATTTATGCACTATTTCAACCGGGGTAAAC	943
QY	241 ArgIlyValAlaThrGluPheGluSerPheSerPheAspAlaThrPheHisAlaIlySylS	260
DB	944 CGAAGGTGGCAACAGATTTGAGTCTTTTCCCTTACCGCTACTTTTCAATGCAAAAGAA	1003

Qy 261 GlnlleProCysIleValSerMetLeuThrIysGluLeuTyrPheTyrHis 277  
Db 1004 CAGATTCACGTATGTTTCCATGCTCACAAAGAACTCTATTATTATAC 1054

RESULT 5  
US-08-462-969B-3  
Sequence 3, Application US/08462969B  
Patent No. 6087150  
GENERAL INFORMATION:  
APPLICANT: He, Wei-Wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
TITLE OF INVENTION: Like Apoptosis Protease 3 and 4  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,969B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/334,251  
FILING DATE: 11-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PFI40P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1159 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-462-969B-3

Alignment Scores:  
Pred. No.: 1.97e-280 Length: 1159  
Score: 277.00 Matches: 277  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-613-508B-4 (1-277) x US-08-462-969B-3 (1-1159)

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Qy 41 TyrProGluMetGlyLeuCysIleIleIleAsnAsnLysAsnProHisLysSerThrGly 60  
Db 343 TATCTCTGAGATGGGTTTATGATATATATATATATATATATATATATATATATATATAT 402

Qy 61 MetThrSerArgSerGlyThrAspValAspAlaAsnLeuAspGluThrPheArgAsn 80  
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Db 463 TTGAAATATGAGCTCAGAAATGAAATGATCTTACGCTGAAGAAATTTGGAAATTTGAG 522

Qy 101 ArgAspValSerIysGluAspHisSerIysArgSerSerPheValCysValLeuLeuSer 120  
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Qy 121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuLysIleThr 140  
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Qy 141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyLysProLysLeuPheIleIle 160  
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Qy 161 GlnAlaCysArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAsp 180  
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RESULT 6  
US-09-124-934A-3  
Sequence 3, Application US/09124934A  
Patent No. 6495519  
GENERAL INFORMATION:  
APPLICANT: He, Wei-Wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3  
FILE REFERENCE: PFI40C1  
CURRENT APPLICATION NUMBER: US/09/124,934A  
CURRENT FILING DATE: 1994-11-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 1159  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-124-934A-3

Alignment Scores:  
Pred. No.: 1.97e-280 Length: 1159  
Score: 277.00 Matches: 277  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-613-508B-4 (1-277) x US-09-124-934A-3 (1-1159)

Qy 1 MetGluAsnThrGluAsnSerValAspSerIysSerIleValAsnLeuGluProLysIle 20  
Db 223 ATGGAGAACACTGAAACCTCAGTGGATTCAAAATCTATAAAATTTGGAAACCAAGATC 282

QY	21	LEHSGLSERGLSERMETASPSEGLYIESERLEUAAPASSETYLYMETHASP	40
Db	283	ARACATGAGGCAATTCATGACCTCTGGAAATATCCCTGGACMACGTTATPAAATGGAT	342
QY	41	TYPROGLUMETGLYLEUCYSILEILEIENASENLYSASPHEHISLYSESTHRGILY	60
Db	343	TATCCGATGATGGGTTATGTTATATTAATTAATTAAGAAATTTTCATAAAAGCACTGGA	402
QY	61	MECTHRSEARYSERGLYTHRASPVALASPAIAAIAENLEUARGGLUTHRPHETARGSN	80
Db	403	ARGACATCTCCGGTCGGTACAGATGTCATGACGAAACCTCAGGAGAACCTTCAGAAAC	462
QY	81	LEULSYTYGILVALARASNLYSASNPSEUTRRARGGLUGILILEVALGILEUMET	100
Db	463	TTGAAATATGAGTCAAGGATPAAATATGATCTTACACGTGAAGAAATGTGGAATTCATG	522
QY	101	ARGASPVALSERLYSGILUASPHISSERTYSARGSESPHEVALCYVALLEUENSER	120
Db	523	CCTGATGTTCTTAAAGAAAGATCACAGCAAAAGGACACTTTTGTGTGTCTCTGAGC	582
QY	121	HISGLYGLUGLUGLYILEIIEPHEGLYTHRANGLYPROVALASPLEUYLEYILETHR	140
Db	583	CATGCTGAGAGGAGATATATTTTGGAACAATGACCTGTGTGACCTTAATAAATAACA	642
QY	141	ASPHEPHEARGGLYASPARGYCYSARGSERLEUTRGILYLYSPOLYSLEUPHEHILEI	160
Db	643	AACITTTTCAGAGGGGATCGTTGTGAGAGTCTTACTGSAACCAACCTTTTCATTATTT	702
QY	161	GLINALCYSAARGLYTHRGILUENASPCYSGILYIEGLUTHRASPSERGLYVALASPAR	180
Db	703	CAGGCTCTCCGGTACAGAACTGGACTGTGGCANTGAGACAGACAGTGGTGTGATGAT	762
QY	181	ASPMEALACYSHEHISLYLEPROVALGILUASPHLEULYRAATYSERETHALA	200
Db	763	GACATGSGGTGTCATPAAATATCCAGTGAAGCCGACCTCTGTATGATGACTCCACAGCA	822
QY	201	PROGLYTYRYSERTRIPARGANSERTYASPSGLYSERTYPHEILEGLNSERLEUCYS	220
Db	823	CCTGGTTATTTATCTCTGGCGAAATTCAGAGATGGCTCTCTGTCATCCAGTCCCTTGT	882
QY	221	ALAMETLEULYSGILTYRALASPLYSLENGUNPHEHISILEUETHRARGVALASN	240
Db	883	GCCATGCTGAAACAGATATGCCGACACAGCTTGATTAATGACATCTTACCCGGGTTAAC	942
QY	241	ARGLYSVALAATHRGILUPHEGLUSERPHEASERPHESAPAAATRRPHEHISALILEULYS	260
Db	943	CGAAAGGTGGCAACGAATTTGAGTCTTTCTTTGACGCTACTTTTCAGGCAAGAA	1002
QY	261	GLINLEPROCYSILEVALSERMETEURTHIRYSGILUENLYTYRPHETYRHS	277
Db	1003	CAGATTCATGATGTGTTTCCATGCTCACAAAAGAACCTTTTATTATCAC	1053
RESULT 7			
US-08-334-251D-3			
/ Sequence 3, Application US/08334251D			
/ Patent No. 6538121			
/ GENERAL INFORMATION:			
/ APPLICANT: He et al.			
/ TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 and			
/ FILE REFERENCE: PFI40			
/ CURRENT APPLICATION NUMBER: US/08/334, 251D			
/ CURRENT FILING DATE: 1994-11-01			
/ NUMBER OF SEQ ID NOS: 12			
/ SOFTWARE: PatentIn version 3.0			
/ SEQ ID NO 3			
/ LENGTH: 1159			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
US-08-334-251D-3			
Alignment Scores:			
Pred. No.: 1,97e-280			
Length: 1159			

[illegible]

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Boehringer Ingelheim Corporation  
STREET: 900 Ridgebury Road, P.O. Box 368  
CITY: Ridgefield  
STATE: Connecticut  
COUNTRY: United States of America  
ZIP: 06877-0368  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processing  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,297A  
FILING DATE: 27-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/038,266  
FILING DATE: 28-Feb-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert P. Raymond  
REGISTRATION NUMBER: 25089  
REFERENCE/DOCKET NUMBER: 9/121PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-791-6183  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 904  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
DESCRIPTION: DNA  
FEATURE:  
NAME/KEY: chimeric gene TNFp120 AIG.1  
OTHER INFORMATION: residues 1 to 139 comprise the  
promoter sequence; residues 140 to 151, the linker  
the remaining residues comprise the AIG.1 sequence  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-032-297A-4  
Alignment Scores:  
Pred. No.: 1.8e-210 Length: 904  
Score: 210.00 Matches: 248  
Percent Similarity: 99.20% Conservative: 0  
Best local Similarity: 99.20% Mismatches: 1  
Query Match: 75.81% Indels: 2  
DB: 4 Gaps: 0  
US-09-613-508b-4 (1-277) x US-09-032-297A-4 (1-904)  
QY 29 SerGlyIleSerLeuAspAsnSerTyrIleMetAspTyrProGluMetGlyLeuCysIle 48  
DB 155 TCTGGAAATATCCCTGGACACAGTTATATAAATGATTAATCTCTGAGATGGGTTATATATA 214  
QY 49 IleIleAsnAsnLysAsnPheHisLysSerThrGlyMetThrSerArgSerGlyThrAsp 68  
DB 215 ATATATATATATAGAAATTTTCATTAAGACCTGGAATGACATCTCGCTCGACAGAT 274  
QY 69 ValAspAlaIleAsnLeuArgGluThrPheArgAsnLeuLysTyrGluValArgAsnLys 88  
DB 275 GTCCGATCGACCAACCTCAGGAAACATTCAGAACTTGAAATATGAAGTCAGGAATAAA 314  
QY 89 AsnAspLeuThrArgGluGluIleValGluMetArgAspValSerLysGluAsnHis 108  
DB 335 AATGATCTTACACGTAAGAAATTTGTAATGATGCGTGTGTTCTTAAGAGAGATCAC 394  
QY 109 SerLysArgSerSerPheValCysValLeuLeuSerHisGlyGluGluGlyIleIlePhe 128  
DB 395 AGCAAAAGACGACGATTTTGTGTGTGTCTGAGCCATGCTGAAGAAGATATATTTT 454  
QY 129 GlyThrAsnGlyProValAspLeuLysLysIleThrAsnPheArgGlyAspArgCys 148

DB 455 GGACAAATAGACCTGTGACCTGAAAAAATAACAACTTTTCAGAGGGATGCTGT 514  
QY 149 ArgSerLeuThrGlyLysProLysLeuPheIleIleGlnAlaCysArgGlyThrGluLeu 168  
DB 515 AGAAGCTAACTGAGAAACCAACTTTTCATTAATTCAGGCTGCGGTGTACAAACTG 574  
QY 169 AspCysGlyIleGluThrAspSerGlyValAspAspAspMetAlaCysHisLysIlePro 188  
DB 575 GACTGTGCAATTGACACACAGTGTGTGATGATGACATGCGGTGTATATAAATACCA 634  
QY 189 ValGluAlaAspPheLeuTyrAlaTyrSerThrAlaProGlyTyrTyrSerTrpArgAsn 208  
DB 635 GTGAGAGCCGACCTCTTGTATGCATACACAGACACCTGTTATATTTCTGGCAAT 694  
QY 209 SerLysArgGlySerTrpPheIleGlnSerLeuCysAlaMetLeuLysGlnTyrAlaAsp 228  
DB 695 TCAAAGATAGCTCCGCTGTCATCCAGTCGCTTTGCGCATCTGAAACAGATGCCGAC 754  
QY 229 LysLeuGluPheMetHisIleLeuThrArgVal-AsnArgLysValAlaThrGluPheG1 248  
DB 755 AACCTGAAATTTATGACATCTTTACCCGGGC-TAACCAAAAGTGCGCAACGAATTGA 813  
QY 248 uSerPheSerPheAspAlaThrPheHisAlaLysLysGlnIleProCysIleValSerMet 268  
DB 814 GTCCCTTTCTCTTACGCTACTTTTCATCAACAAAGAAAGATTCATGATGTTCCAT 873  
QY 268 LeuThrLysGluLeuTyrPheTyrHis 277  
DB 874 GCTCAAAAGAACTCTATTATTATCAC 901  
RESULT 9  
US-09-032-297A-6  
Sequence 6, Application US/09032297A  
Patent No. 6525184  
GENERAL INFORMATION:  
APPLICANT: Randal J. Tate, Steven D. Marlin and  
Randal W. Barton  
TITLE OF INVENTION: Self-Regulated Apoptosis of  
Inflammatory Cells by Gene Therapy  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Boehringer Ingelheim Corporation  
STREET: 900 Ridgebury Road, P.O. Box 368  
CITY: Ridgefield  
STATE: Connecticut  
COUNTRY: United States of America  
ZIP: 06877-0368  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processing  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,297A  
FILING DATE: 27-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/038,266  
FILING DATE: 28-Feb-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert P. Raymond  
REGISTRATION NUMBER: 25089  
REFERENCE/DOCKET NUMBER: 9/121PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-791-6183  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1789  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>



DESCRIPTION: DNA  
FEATURE:  
NAME/KEY: chimeric gene TNFp1005 AIG.1  
OTHER INFORMATION: residues 1 to 1023 comprise the  
promoter sequence, residues 1024 to 1036, the linker sequence,  
and the remaining residues comprise the AIG.1 sequence  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-032-297A-6  
Alignment Scores:  
Pred. No.: 3.4e-210 Length: 1789  
Score: 210.00 Matches: 248  
Percent Similarity: 99.20% Conservative: 0  
Best Local Similarity: 99.20% Mismatches: 1  
Query Match: 75.81% Indels: 2  
DB: 4 Gaps: 0  
US-09-613-508B-4 (1-277) x US-09-032-297A-6 (1-1789)  
QY 29 SerGlyIleSerLeuAspAsnSerTyrlYmechAspTyrlProGluMetGlyLeuCySile 48  
DB 1040 TCTGGAAATATCCCGGACACAGTTAATAATGATATCTAGATGGTTTATATGATA 1099  
QY 49 IleIleAsnAsnLysAsnPhenHisLysSerThrGlyMetThrSerArgSerGlyThrAsp 68  
DB 1100 ATATTATATATAGAAATTTTCATTAAGACATGGAATGACATCTCGTCTGGTACAGAT 1159  
QY 69 ValAspAlaAlaAsnLeuArgGluThrPheArgAsnLeuLysTyrlGluValArgAsnLys 88  
DB 1160 GTGATGACAGAACTTCAGGAAACATTCAGAACTTGAAATGAAATGACAGAAATAA 1219  
QY 89 AsnAspLeuThrArgGluGluIleValGluLeuMetArgAspValSerLysGluAspHis 108  
DB 1220 AATGATCTTACAGTGAAGAAATGTGGAATGTATGCGTATGTTCTAAGAAGATCAC 1279  
QY 109 SerLysArgSerSerPheValCysValLeuLeuSerHisGlyGluGluIleIlePhe 128  
DB 1280 AGCAAAAGAGCACTTTTGTGTGCTCTGAGCATGCTGAGAGAGAAATATATTTT 1339  
QY 129 GlyThrAsnGlyProValAspLeuLysLysIleThrAsnPheArgGlyAspArgCys 148  
DB 1340 GGAAACAAATGACCTGTTGACCTGAAACAAATTTTTCAGAGGGGAAATCGTGT 1399  
QY 149 ArgSerLeuThrGlyLysProLysLeuPheIleIleGlnIleAcysArgGlyThrGluLeu 168  
DB 1400 AGAAGTCTAAGTGAACCAACCACTTTTCAATTAATTCAGCCCTGCGTGTACAGAACTG 1459  
QY 169 AspCysGlyIleGluThrAspSerGlyValAspAspMetAlaCysHisLysIlePro 188  
DB 1460 GACGTGTGCATTTGAGACAGACAGTGTGATGATGACATGCGTGTCTAATAAATACCA 1519  
QY 189 ValGluAlaAspPheLeuTyrlAlaTyrlSerThrAlaProGlyTyrlTyrlSerThrArgAsn 208  
DB 1520 GTGAGGCGCACTTCTTGTATGCACTTCAACAGACCTGTTATTTTCTTGGCGAAAT 1579  
QY 209 SerLysAspGlySerTrpPheIleGlnSerLeuCysAlaMetLeuLysGlyTyrlAlaAsp 228  
DB 1580 TCAAGATGCGCTCTGTCATCAGTCCGCTTTGTGCCATGCGAAACGATATGCCGAC 1639  
QY 229 LysLeuLupPheMetHisIleLeuThrArgVal-AsnArgLysValAlaThrGluPheG 248  
DB 1640 AAGCTTAATTTAAGCAATTTTCAACCCGGGC-TAACCGAAAGGTGCAACAAATTTTG 1698  
QY 248 UsePheSerPheAspAlaThrPheHisAlaLysLysGlnIleProCysIleValSerPhe 268  
DB 1699 GTCTTTTCTTCAACCTTCTTTCATGCAAGAAACAAATTCATGATTTTCTTCAT 1758  
QY 268 tLeuThrLysGluLeuTyrlPheTyrlHis 277  
DB 1759 GCTCAAAAGAACTATATTTTATCAC 1786  
RESULT 10  
US-09-032-297A-5

Sequence 5, Application US/09032297A  
Patent No. 6525184  
GENERAL INFORMATION:  
APPLICANT: Revati J. Tatake, Steven D. Marlin and  
Randall W. Barton  
TITLE OF INVENTION: Self-Regulated Apoptosis of  
Inflammatory Cells by Gene Therapy  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Boehringer Ingelheim Corporation  
STREET: 900 Ridgebury Road, P.O. Box 368  
CITY: Ridgefield  
STATE: Connecticut  
COUNTRY: United States of America  
ZIP: 06877-0368  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processing  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,297A  
FILING DATE: 27-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/038,266  
FILING DATE: 28-FEB-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert P. Raymond  
REGISTRATION NUMBER: 25089  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: 9/121PCT  
TELEPHONE: 203-791-6183  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1490  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
DESCRIPTION: DNA  
FEATURE:  
NAME/KEY: chimeric gene TNFp706 AIG.1  
OTHER INFORMATION: residues 1 to 724 comprise the  
promoter sequence; residues 725 to 736, the linker sequence, and  
the remaining residues comprise the AIG.1 sequence  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-032-297A-5  
Alignment Scores:  
Pred. No.: 1.71e-192 Length: 1490  
Score: 193.00 Matches: 193  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.68% Indels: 0  
DB: 4 Gaps: 0  
US-09-613-508B-4 (1-277) x US-09-032-297A-5 (1-1490)  
QY 29 SerGlyIleSerLeuAspAsnSerTyrlYmechAspTyrlProGluMetGlyLeuCySile 48  
DB 740 TCTGGAAATATCCCGGACACAGTTAATAATGATATCTAGATGGTTTATATGATA 799  
QY 49 IleIleAsnAsnLysAsnPhenHisLysSerThrGlyMetThrSerArgSerGlyThrAsp 68  
DB 800 ATATTATATATAGAAATTTTTCATTAAGACATGGAATGACATCTCGTCTGGTACAGAT 859  
QY 69 ValAspAlaAlaAsnLeuArgGluThrPheArgAsnLeuLysTyrlGluValArgAsnLys 88  
DB 860 GTGATGACAGAACTTCAGGAAACATTCAGAACTTGAAATGAAATGAGTCAAGCAATAAA 919  
QY 89 AsnAspLeuThrArgGluGluIleValGluLeuMetArgAspValSerLysGluAspHis 108

Db 920 AATGATCTTACACGTGAGAAATTGTGGAAATTGAGCGTATGTTCTTAAAGAGATCAC 979  
Qy SerIysArgSerPheValCysValIleuSerHisGlyIugIlePhe 128  
Db 960 AGCAAAAGACGACGTTTGTGTGCTTGTGACCAAGGTGAGAAAGGATATTTT 1039  
Qy 129 GlyThrAenGlyProValAspLeuLysLysIleThrAspPheArgGlyAspArgCys 148  
Db 1040 GGAACAAATGACCGTTGACCTGAAATAAACAACCTTTTCAAGAGGAGATCGTGT 1099  
Qy 149 ArgSerLeuThrGlyLysProLysLeuPheIleIleGlnIleCysArgGlyThrGluLeu 168  
Db 1100 AGAAGTCACTGAGAAACCAACCTTTCTATTTCAGGCTGCTCGGTGACGAACTG 1159  
Qy 169 AspCysGlyIleGlnThrAspSerGlyValAspAspMetAlaCysHisLysIlePro 188  
Db 1160 GACTGTGGCATTGAGACAGACAGAGTGGTGTATATGATGAGGGTGTCATTAATATCCA 1219  
Qy 189 ValGlnAlaAspPheLeuThrAlaTyrSerThrAlaProGlyTyrTyrSerTyrArgAsn 208  
Db 1220 GTGGAGGCGCACTCTTGTATGCAATCTCCACAGCACCTGGTTATATCTTGGCGAAAT 1279  
Qy 209 SerIysAspGlySerTyrPheIleGlnSerLeuCysAla 221  
Db 1280 TCAAGATGAGCTCTGCTTCATCCAGTCGCTTGTGTGC 1318

## RESULT 11

US-09-561-756-10  
; Sequence 10, Application US/09561756  
; Patent No. 6376226  
; GENERAL INFORMATION:  
; APPLICANT: Alnemur, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/561,756  
; CURRENT FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 09/227,721  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 835  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(835)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-561-756-10

## Alignment Scores:

Pred. No.: 1,53e-188 Length: 835  
Score: 189.00 Matches: 276  
Percent Similarity: 99.28% Conservative: 0  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 68.23% Indels: 2  
DB: 4 Gaps: 0

US-09-613-508b-4 (1-277) x US-09-561-756-10 (1-835)

Qy 1 MetGluAsnThrGluAsnSerValAspSerLysSerIleLysAsnLeuGluProLysIle 20  
Db 1 ATGGAGAACACTGAAACCTGAGTTCAAATCCATTAAATTTGGAACCAAAATC 60  
Qy 21 ILeHisGlySerGluSerMetAspSerGlyLysSerLeuAspAsnSerTyrLysMetAsp 40  
Db 61 ATACATGGAAGCAATCAATGACTGTGAATATCCCTCGACACACAGTATTAATGAT 120  
Qy 41 TyrProGluMetGlyLeuCysIleIleIleAsnAsnLysAsnProHisLysSerThrGly 60  
Db 121 TATCTGATGATGGTTTATGATATATATATATATTAAGAAATTTTCATTAAGACACGCGA 180

Qy 61 MetThrSerArgSerGlyThrAspValAspAlaAlaAsnLeuArgLysThrPheArgAsn 80  
Db 181 ATGACATCTCGGCTCTGTTACAGATGTCATGACGAAACCTCAGGAAACATTCGAAAC 240  
Qy 81 LeuLysTyrGluValArgAsnLysAsnAspLeuThrArgGluIleValGluLeuMet 100  
Db 241 TTGAATATGAAGTCAAGAAATATAATATCTTACACGTAAGAAATGTGGAAATGTATG 300  
Qy 101 ArgAspValSerLysGluAspHisSerLysArgSerPheValCysValIleuSer 120  
Db 301 CGTATGTTTCTTAAGAAATACAGCAAAAGAGAGGTTTGTGTGCTTCTGAC 360  
Qy 121 HisGlyIugIleIleIlePheGlyThrAenGlyProValAspLeuLysLysIleThr 140  
Db 361 CATGGGAAGAGAAATATATTTTGGAACTATGACCGTTGACCTGAAAAAATPACA 420  
Qy 141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyLysProLysLeuPheIle 160  
Db 421 AACTTTTACAGGGGATGTGTGAGAGTCACTGCAATGGAACCAAACTTTTCAATAT 480  
Qy 161 GlnAlaCysArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAsp 180  
Db 481 CAGGCTGCGCTGTGTACAGAACTGACCTGTGCATTGACACAGACAGTGTTATGAT 540  
Qy 181 AspMetAlaCysHisLysIleProValGlu-AlaAspPheLeuThrAlaTyrSerThrAl 200  
Db 541 GACATGCGCTGTCATTAATATACAGTGA-TGCCACTTCTGTATGATCTCACAGC 599  
Qy 200 AbProGlyTyrTyrSerTyrArgAsnSerLysAspGlySerTyrPheIleGlnSerLeu 220  
Db 600 AACTGTATATATCTTGTGGAATTCAAAGATGCTCTGTTCATCCAGTCGCTTGTG 659  
Qy 220 SalMetLeuLysGlnTyrAlaAspLysLeuGluPheMetHisIleLeuThrArgValAs 240  
Db 660 TGCCATGCTGAAAGACGTATGCCAGACCTTGAATTTATGCACTTCAACCGGTTAA 719  
Qy 240 nArgLysValAlaThrGluPheGluSerPheSerPheAspAlaThrPheHisAlaLys 260  
Db 720 CCGAAAGGTGGCAACGAATTTGAGCTTTTCCCTTGTGACCTACTTTTCATGCAAGAA 779  
Qy 260 sGlnIleProCysIleValSerMetLeuThrLysGluLeuTyrPheTyrHis 277  
Db 780 ACAGATTCATGATATTTTCCATGCTCACAAAGAACCTATATTTATCAC 831

## RESULT 12

US-09-227-721-10  
; Sequence 10, Application US/09227721  
; Patent No. 6379950  
; GENERAL INFORMATION:  
; APPLICANT: Alnemur, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/227,721  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 835  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(835)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-227-721-10

## Alignment Scores:

Pred. No.: 1,53e-188 Length: 835  
Score: 189.00 Matches: 276  
Percent Similarity: 99.28% Conservative: 0  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 68.23% Indels: 2

DB: 4 Gaps: 0  
US-09-613-508b-4 (1-277) x US-09-227-721-10 (1-835)

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QY 1 MetGluSerThrGluAsnSerValAspSerIleLeuAsnLeuGluProlysis 20
DB 1 ATGGAACACACTGAAACTCAGTGAATCAAAATCCATTAAATTTGGAACCAAGATC 60
QY 21 ILeuGlySerGluSerMetAspSerGlyIleSerLeuAsnSerIleValGluMetAsp 40
DB 61 ATACATGGAACGATCAATGACTCTGGAATATCCCTGGAACAACATTAATAAAGAT 120
QY 41 TyrProGluMetGlyLeuGlyIleIleLeuAsnLeuAsnPheHisIleSerThrGly 60
DB 121 TATCTGAGATGGGTTTATGTAATAATAATAATAAGATTTCTATAAAGACACGA 180
QY 61 MetThrSerArgSerGlyThrAspValAspAlaIleAsnLeuArgGluThrPheArgAsn 80
DB 181 ATGACATCTCGATCTGGTACAGATGTCAGTCAACCAACCTCAGGGAACATTCAGAAC 240
QY 81 LeuIleValGluValArgAsnLeuAsnAspLeuThrArgGluGluIleValGluLeuMet 100
DB 241 TTGAATATGAAAGCAAGATTAATAATGATCTTACGCTGGAAGAAATTTGGAAATGATG 300
QY 101 ArgAspValSerIleGluAspHisSerIleSerArgSerPheValCysValLeuLeuSer 120
DB 301 CGTATGTTTAAAGAAATCAGCAAGCAAGCAAGTCTTTGTTGCTGCTCTGAGC 360
QY 121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuIleValIleThr 140
DB 361 CATGCTGAAGAAAGAAATTTTGGACCAATGACCTGTTGACCTGAAATAATATACA 420
QY 141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyValProlysisPheIle 160
DB 421 AACTTTTCAAGGGGATCGTTGAGAGCTTAACTGGAACCAACCACTTTTCAATATT 480
QY 161 GlnAlaCysArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAsp 180
DB 481 CAGGCTGCCCGTACAGAACTGAGCTGTCGATGAGACAGACAGAGTGTGATGAT 540
QY 181 AspMetAlaCysHisIlePheProValGlu-AlaAspPheLeuThrAlaIleSerThrAl 200
DB 541 GACATGCGGTGTCAATAAATCCAGTGA-TGCCCACTTCTGTGATGATCTCCACAGC 599
QY 200 AspGlyTyrTyrSerThrArgAsnSerIleAspGlySerThrPheIleGlnSerLeuCy 220
DB 600 AACTGTTATTTCTTGGCAATTCGAAGATGCTCCCTGCTCATCCCGGCTTGG 659
QY 220 SalMetLeuIleGlnTyrAlaAspIleLeuGluPheMetHisIleLeuThrArgValAs 240
DB 660 TGCCATGCTGAACAGTATGCGCAAGCTTGAATTTATGACATTTTACCCCGGTTAA 719
QY 240 NArgIleValAlaIleThrGluPheGluSerPheSerPheAspAlaThrPheHisAlaIleVal 260
DB 720 CCGAAGGTGGCAACGAATTTGAGTCTTTTCTTTACGCTACTTTTCAAGCAAGAA 779
QY 260 sGlnIleProCysIleValSerMetLeuThrIleGluLeuTyrPheIleHis 277
DB 780 ACGATTCAATGATTTGTTCCATGCTCAAAAGAACTCTATTTTATCAC 831

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/ LENGTH: 2635
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (225) ... (1058)
/ US-09-484-617-3

Alignment Scores:
Pred. No.: 4,436-188 Length: 2635
Score: 189.00 Matches: 276
Percent Similarity: 99.28% Conservative: 0
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 68.23% Indels: 2
DB: 4 Gaps: 0

US-09-613-508b-4 (1-277) x US-09-484-617-3 (1-2635)
QY 1 MetGluSerThrGluAsnSerValAspSerIleLeuAsnLeuGluProlysis 20
DB 225 ATGGAACACACTGAAACTCAGTGAATCAAAATCCATTAAATTTGGAACCAAGATC 284
QY 21 ILeuGlySerGluSerMetAspSerGlyIleSerLeuAsnSerIleValGluMetAsp 40
DB 285 ATACATGGAACGATCAATGACTCTGGAATATCCCTGGAACAACATTAATAAAGAT 344
QY 41 TyrProGluMetGlyLeuGlyIleIleLeuAsnLeuAsnPheHisIleSerThrGly 60
DB 345 TATCTGAGATGGGTTTATGTAATAATAATAATAAGATTTCTATAAAGACACGA 404
QY 61 MetThrSerArgSerGlyThrAspValAspAlaIleAsnLeuArgGluThrPheArgAsn 80
DB 405 ATGACATCTCGATCTGGTACAGATGTCAGTCAACCAACCTCAGGGAACATTCAGAAC 464
QY 81 LeuIleValGluValArgAsnLeuAsnAspLeuThrArgGluGluIleValGluLeuMet 100
DB 465 TTGAATATGAAAGCAAGATTAATAATGATCTTACGCTGGAAGAAATTTGGAAATGATG 524
QY 101 ArgAspValSerIleGluAspHisSerIleSerArgSerPheValCysValLeuLeuSer 120
DB 525 CGTATGTTTCAAGAAATCAGCAAGCAAGCAAGTCTTTGTTGCTGCTCTGAGC 584
QY 121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuIleValIleThr 140
DB 585 CATGCTGAAGAAAGAAATTTTGGACCAATGACCTGTTGACCTGAAATAATATACA 644
QY 141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyValProlysisPheIle 160
DB 645 AACTTTTCAAGGGGATCGTTGAGAGCTTAACTGGAACCAACCACTTTTCAATATT 704
QY 161 GlnAlaCysArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAsp 180
DB 705 CAGGCTGCCCGTACAGAACTGAGCTGTCGATGAGACAGACAGAGTGTGATGAT 764
QY 181 AspMetAlaCysHisIlePheProValGlu-AlaAspPheLeuThrAlaIleSerThrAl 200
DB 765 GACATGCGGTGTCAATAAATCCAGTGA-TGCCCACTTCTGTGATGATCTCCACAGC 823
QY 200 AspGlyTyrTyrSerThrArgAsnSerIleAspGlySerThrPheIleGlnSerLeuCy 220
DB 824 AACTGTTATTTCTTGGCAATTCGAAGATGCTCCCTGCTCATCCCGGCTTGG 883
QY 220 SalMetLeuIleGlnTyrAlaAspIleLeuGluPheMetHisIleLeuThrArgValAs 240
DB 884 TGCCATGCTGAACAGTATGCGCAAGCTTGAATTTATGACATTTTACCCCGGTTAA 943
QY 240 NArgIleValAlaIleThrGluPheGluSerPheSerPheAspAlaThrPheHisAlaIleVal 260
DB 944 CCGAAGGTGGCAACGAATTTGAGTCTTTTCTTTTGAAGCTACTTTTCAAGCAAGAA 1003
QY 260 sGlnIleProCysIleValSerMetLeuThrIleGluLeuTyrPheIleHis 277
DB 1004 ACGATTCAATGATTTGTTCCATGCTCAAAAGAACTCTATTTTATCAC 1055

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RESULT 14  
US-08-964-308-9  
Sequence 9, Application US/08964308  
Patent No. 6066715  
GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: ZAMONT, ROBERT  
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
TITLE OF INVENTION: BINDING ASSAY  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,308  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: NORTH, ROBERT J.  
REGISTRATION NUMBER: 27,366  
REFERENCE/DOCKET NUMBER: 19840 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-7262  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1001 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-964-308-9  
Alignment Scores:  
Pred. No.: 7.09e-175 Length: 1001  
Score: 176.00 Matches: 276  
Percent Similarity: 99.28% Conservative: 0  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 63.54% Indels: 2  
DB: Gaps: 0  
US-09-613-508b-4 (1-277) x US-08-964-308-9 (1-1001)  
QY 1 MetGluSenThrgLusAsnSerValAspSerLysSerIleLysAsnLeuGluProLysIle 20  
DB 64 ATGAGAACTGTAAGAACTGATGATTCATAATCCATTAAATTTGGACCAACCAATC 123  
QY 21 ILeHisGlySerGluSerMetAspSerGlyIleSerLeuAspAsnSerIlyLysMetAsp 40  
DB 124 ATACATGGAAGCAGATCAATGACTCTGGAATATCCCTGGACCAACAGTTTAAATGAT 183  
QY 41 TyrProGluMetGlyLeuGlyCysIleIleLeuAsnAsnLysAsnProHisGlySerThrGly 60  
DB 184 TATCTCGATGAGGAGTTAT 243  
QY 61 MetHisSerArgSerGlyThrAspValAspAlaIleAsnLeuArgGluThrPheArgAsn 80  
DB 244 ATGACATCTCGCTGTGTGACAGATGTGATGACCAACCTCAGGAAACATTCCAGAAC 303  
QY 81 LeuLysTyrGluValAlaArgAsnLysAsnAspLeuThrArgGluGluIleValGluLeuMet 100

DB 304 TTGAATATGAGTCAGCAATTAATAATGATCTTACACGTGAAGAATTTGGAATTGATG 363  
QY 101 ArgAspValSerLysGluAspHisSerLysArgSerSerPheValCysValLeuLeuSer 120  
DB 364 CGTGATGTTTCAAGAAAGATCAGCAAAAGAGACAGATTGTTGTGTGCTCTGAGC 423  
QY 121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuLysIleLeuThr 140  
DB 424 CAGTGGAAGAGATATATTTTGGACCAATGACCTGTGACCTGAAAAATAACA 483  
QY 141 AsnPheAspArgLysAspArgCysArgSerLeuThrGlyLysProLysLeuPheIleIle 160  
DB 484 AACTTTTCAGAGGGGAGTGTGTGAGAGTCAATGGAAGAAACCAACTTTCTATT 543  
QY 161 GluAlaCys-ArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAs 180  
DB 544 CAGGCTCTC-CCGTGGTACAGAACTGACTGTGTCATTGACACAGACAGTGGTGTGATGA 602  
QY 180 PAspMetAlaCysHisLysIleProValGluAlaAspPheLeuThrAlaIlySerThrAl 200  
DB 603 TGCATGGGCTGCTAATAATCCAGTGAAGCCAGCTTGTGTATGATCACTCCACAGC 662  
QY 200 AProGlyTyrIlySerTyrPargAsnSerLysAspLysSerTyrPheIleGlnSerLeuCy 220  
DB 663 ACCTGGTATTATTTCTGGCGAATTCAAAGATGCTCCTGGTTCATCCAGTCCCTTG 722  
QY 220 saIaMetLeuLysGlnTyrAlaAspLysLeuGluPheMetHisIleLeuThrArgValAs 240  
DB 723 TCCCATGCTGAAGACGATATGCGACAGACCTGGAATTATGACATTCATCCGGGTTRA 782  
QY 240 nArgLysValAlaThrGluPheGluSerPheSerPheAspAlaThrPheHisAlaLysGly 260  
DB 783 CCGAAGGTGGCAACGAAATTGAGTCTTTTCTTTGACGCTATTTTCATGCAAGAA 842  
QY 260 sGlnIleProCysIleValSerMetLeuThrLysGluLeuTyrPheTyrHis 277  
DB 843 ACAGATTCATGATTTGTTTCATGCTCACAAGAAAGACCTATTTTATCAC 894  
RESULT 15  
US-08-964-313-9  
Sequence 9, Application US/08964313  
Patent No. 6114132  
GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: GRESSER, MICHAEL  
APPLICANT: KENNEDY, BRIAN  
APPLICANT: NICHOLSON, DONALD  
APPLICANT: RAMACHANDRAN, CHIDAMBARAN  
APPLICANT: SMOREY, KATHRYN  
APPLICANT: FORD-HUTCHINSON, ANTHONY  
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,313  
FILING DATE: 04-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: 60/030,408  
FILING DATE: 04-NOV-1996  
APPLICATION NUMBER: PCT/CA97/00825

FILING DATE: 03 -NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DURETTE, PHILIPPE L.  
 REGISTRATION NUMBER: 35,125  
 REFERENCE/DOCKET NUMBER: 19824Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4568  
 TELEFAX: 732-594-4720  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1001 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-964-313-9

Alignment Scores:  
 Pred. No.: 7,09e-175 Length: 1001  
 Score: 176.00 Matches: 276  
 Percent Similarity: 99.28% Conservative: 0  
 Best Local Similarity: 99.28% Mismatches: 1  
 Query Match: 63.54% Indels: 2  
 DB: 3 Gaps: 0

US-09-613-508b-4 (1-277) x US-08-964-313-9 (1-1001)

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DB      64 ATGGAGAACCTGTAAGACCTGATGAGATTCCTTAATTAATTTGGACCAAGATC 123
QY      21 IleHisGlySerGluSerMetAspSerGlyIleSerLeuAspAsnSerTyrIleMetAsp 40
DB      124 ATACATGAGAGCGAATCATGACCTCGAATATCCCTGACACACGTTATTAATGAT 183
QY      41 TyrProGluMetGlyLeuCysIleIleIleAsnAsnLysAsnPheHisIleSerThrGly 60
DB      184 TATCTGAGATGGGTTTATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 243
QY      61 MetThrSerArgSerGlyThrAspValAspAlaIleAsnLeuArgGluThrPheArgAsn 80
DB      244 ATGACATCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY      81 LeuIleTyrGluValArgAsnLysAsnAspLeuThrArgGluGluIleValGluLeuMet 100
DB      304 TTGAATATGAGACGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
QY      101 ArgAspValSerLysGluAspHisSerLysArgSerPheValCysValLeuLeuSer 120
DB      364 CGTATGTTCTTAAGAGATCAACAGCAAAAGAGCAGTTTGTGTGCTTCTGAGC 423
QY      121 HisGlyGluGluGlyIleIlePheGlyThrAsnGlyProValAspLeuLysIleThr 140
DB      424 CATGTGAGAGAGAAATTAATTTTGGACCAATGACCTGTGACCTGAAAAAATTAACA 483
QY      141 AsnPhePheArgGlyAspArgCysArgSerLeuThrGlyLysProLysLeuPheIleIle 160
DB      484 AACTTTTCAAGAGGAGATCGTTGTAAGATCTAACTGAAACCCAACTTTTCATTATT 543
QY      161 GluAlaCys-ArgGlyThrGluLeuAspCysGlyIleGluThrAspSerGlyValAspAs 180
DB      544 CAGGCTTC-CGTGTGTCAGAACTGACCTGTGCAATGAGACAGAGTGTTGATGA 602
QY      180 PAspMetAlaCysHisIleLysIleProValGluAlaAspPheLeuTyrAlaTyrSerThrAl 200
DB      603 TGAATGCGCGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 662
QY      200 AProGlyTyrTyrSerTyrArgAsnSerLysAspGlySerTyrPheIleGlnSerLeuCy 220
DB      663 ACCGTGTTATATCTTGCGCAAAATCAAGAGATGCTCTGTTCAATCCAGTGGCTTTG 722
QY      220 sAlMetLeuLysGlnTyrAlaAspLysLeuGluPheMetHisIleLeuThrArgValAs 240
  
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DB      723 TGGCATGCTGAACAGTATGCGGACAGCTGAATTTATGACATCTTACCCGGTTAA 782
QY      240 nArgLysValAlaPheGluPheGluSerPheSerPheAspAlaThrPheHisIleLysIle 260
DB      783 CGAAAGGTGCAACAGAAATTTGAGTCTTTCTTGGCCCTACTTTCATGCAAGAA 842
QY      260 sGlnIleProCysIleValSerMetLeuThrLysGluLeuTyrPheTyrHis 277
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